

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2000, 16:43:29 ; Search time 2244.69 Seconds
(without alignments)
3897.314 Million cell updates/sec

Title: US-09-236-468A-1
Perfect score: 2003
Sequence: 1 gtttctctggcagccaag.....atttctctgtgattgttca 2003

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba1:*

2: gb_ba2:*

3: gb_om:*

4: gb_ov:*

5: gb_pat:*

6: gb_ph:*

7: gb_pl1:*

8: gb_pl2:*

9: gb_pr1:*

10: gb_pr2:*

11: gb_pr3:*

12: gb_ro:*

13: gb_sy:*

14: gb_un:*

15: em_fun:*

16: em_hum1:*

17: em_hum2:*

18: em_in:*

19: em_om:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vi:*

30: gb_htg1:*

31: gb_htg2:*

32: gb_in1:*

33: gb_in2:*

34: em_ba1:*

35: em_ba2:*

36: em_hum3:*

37: em_hum4:*

38: gb_pr4:*

39: gb_htg3:*

40: gb_htg4:*

41: gb_htg5:*

42: gb_htg6:*

43: gb_htg7:*

44: em_htg1:*

45: em_htg2:*

46: em_htg3:*

47: em_hum5:*

48: gb_pl3:*

49: gb_pr5:*

50: gb_htg8:*

51: gb_htg9:*

52: gb_htg10:*

53: gb_htg11:*

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55: gb_htg13:*

56: gb_htg14:*

57: gb_in3:*

58: gb_htg15:*

59: gb_htg16:*

60: gb_htg17:*

61: em_htg4:*

62: em_htg5:*

63: em_htg6:*

64: em_htg7:*

65: em_hum6:*

66: gb_htg18:*

67: gb_htg19:*

68: gb_htg20:*

69: gb_htg21:*

70: gb_htg22:*

71: gb_htg23:*

72: gb_vl1:*

73: gb_vl2:*

74: gb_ba3:*

75: em_htg8:*

76: em_htg9:*

77: em_htg10:*

78: em_htg11:*

79: em_htg12:*

80: em_htg13:*

81: em_htg14:*

82: em_htg15:*

83: em_htg16:*

84: em_htg17:*

85: em_htg18:*

86: em_htg19:*

87: em_htg20:*

88: em_htg21:*

89: em_htg22:*

90: em_htg23:*

91: gb_pr6:*

92: gb_pr7:*

93: gb_sts1:*

94: gb_sts2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1942.2	97.0	2641	91 HSU25128	U25128 Human PTH2
2	1942.2	97.0	2641	93 G26909	G26909 human STS S
3	1156.6	57.7	1977	12 RNU55836	U55836 Rattus norv
4	620	31.0	1980	91 HSETHR05	U47129 Human parat
5	620	31.0	159700	39 AC010822	AC010822 Homo sapi
6	620	31.0	173316	43 AC019185	AC019185 Homo sapi
7	594.4	29.7	2429	4 AF132082	AF132082 Danio rer
8	486.4	24.3	2129	4 AF132084	AF132084 Danio rer
9	452.6	22.6	1862	5 I17764	I17764 Sequence 1
10	452.6	22.6	1863	5 I17765	I17765 Sequence 2
11	452.6	22.6	1878	3 OPOPTH	M74445 Opossum par
12	445.2	22.2	1836	12 RATPTH	L19475 Rat parathy

13	445.2	22.2	2051	5	I17766	I17766 Sequence 3
14	445.2	22.2	2065	12	RATPARATHYR	M7184 Rat parathy
15	437.2	21.8	1984	12	NMPHPR	X7936 M.musculus
16	435.6	21.7	2177	3	AF167095	Canis fam
17	432	21.6	1948	92	HUMPHPR	L04308 Human parat
18	430.8	21.5	2067	3	SSU18315	U18315 sus scrofa
19	430.4	21.5	2010	5	I17767	I17767 Sequence 4
20	430.4	21.5	2095	91	HS1767	X68596 H.sapiens m
21	430.4	21.5	2171	91	HSU17418	U17418 Human parat
22	415.6	20.7	2152	4	AF132085	AF132085 Danio rer
23	402.8	20.1	507	12	AF132083	AF132083 Mus muscu
24	197	9.8	234812	40	AC012362	AC012362 Homo sapi
25	189.6	9.5	381	4	MG094326	U94326 Meleagris g
26	176	8.3	1987	4	AF100644	AF100644 Rana ridi
27	166.4	8.3	282	4	AF132081	AF132081 Ictalurus
28	160.4	8.0	1410	3	AF025411	AF025411 Oryctolag
29	159.6	8.0	1703	91	HSU28281	U28281 Human secre
30	158	7.9	1616	91	HSU13989	U13989 Human secre
31	156.4	7.8	1650	91	HSU20178	U20178 Human secre
32	156.2	7.8	1377	5	I28734	I28734 Sequence 1
33	156.2	7.8	2836	3	SSU49434	U49434 Sus scrofa
34	146.2	7.3	2348	92	HUMVAIPR	L20295 Homo sapien
35	146.2	7.3	2754	92	HUMVAIPR	L3288 Human vasoa
36	143.8	7.2	1796	5	E04128	E04128 cDNA encodi
37	143.8	7.2	1796	12	RNSECRS	X59132 R.norvegicu
38	140.4	7.0	548	91	HSPTUR03	U47127 Human parat
39	139.6	7.0	2224	4	AF048819	AF048819 Carassius
40	138.8	6.9	2592	4	CAU56391	U56391 Carassius a
41	137.8	6.9	1654	4	MG031391	U31391 Meleagris g
42	137.8	6.9	2109	4	AB029895	AB029895 Gallus ga
43	137.8	6.9	3129	5	E05551	E05551 DNA encodin
44	137.8	6.9	3129	12	RATVASREC	M86835 Rat vasoaet
45	134.6	6.7	506	4	AF100643	AF100643 Rana ridi

ALIGNMENTS

RESULT	1	HSU25128	2641 bp	PR1	06-JUL-1995
LOCUS		Human PTH2 parathyroid hormone receptor mRNA, complete cds.			
DEFINITION		U25128			
ACCESSION		U25128			
VERSION		U25128.1			
KEYWORDS		GI:887966			
SOURCE		human.			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS		Usdin,T.B., Gruber,C. and Bonner,T.I.			
TITLE		Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor			
JOURNAL		J. Biol. Chem. 270 (26), 15455-15458 (1995)			
MEDLINE		95318121			
REFERENCE		2 (bases 1 to 2641)			
AUTHORS		Bonner,T.I.			
TITLE		Direct Submission			
JOURNAL		Submitted (17-APR-1995) Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg. 36, Room 3A-17, Bethesda, MD 20892-4090, USA			
FEATURES		Location/Qualifiers			
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		/tissue_type="cerebral cortex and hippocampus"			
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		/codon_start=1			
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		/function="stimulates cAMP production in response to parathyroid hormone but not parathyroid hormone-related peptide"			
		/product="PTH2 parathyroid hormone receptor"			
		/protein_id="AAC50157.1"			

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IRMCELPFNSFOGFFVSIYYCNGEVAQAEVKWSPNLSVDWKRTPGGSRRCGS									
VLTVTHSTSSQSVAASTRMVLISGKAAKIASRQPDSSHILPLGYVWNSQDCLPHS									
FHEETKDSGRGQDDILMEKPSRMESNPDTTEGCGQETEDVL"									
polyA_signal 2619..2625									
polyA_site 2641									
BASE COUNT 670 a 564 c 623 g 784 t									
ORIGIN									
Query Match 97.0%; Score 1942.2; DB 91; Length 2641;									
Best Local Similarity 99.0%; Pred. No. 0;									
Matches 1975; Conservative 0; Mismatches 18; Indels 2; Gaps 2;									
QY	10	gggcagccaagttggcatattggaagcttttccgggctctgagaggaggtccctgcttc	59						
DB	63	GGCCAGCCCAAGTTGGCACTTGTCCCGGCTCTGGAGGAGGTCCCTGCTTC	122						
QY	70	ttcctacagcgttcgggcatggcgtggtgggctgcctccacgtctctgggttgc	129						
DB	123	TTCTCTACACCCGTCGCGGCATGGCGGCTGGGGGCTGCCACGTCCTGGGGTTGC	182						
QY	130	taatctcgccagctgctcctggcagagccagctggtattctgagcaccatacta	189						
DB	183	TAATGCTCGCAGCTGCCCTCCTGGCCAGAGCCAGCTGGATTCTGATGSCACCATTA	242						
QY	190	tagagagcagattgtccttctgtgctgaaagcagaagtaacaatgtgaactcaacacag	249						
DB	243	TAGAGAGCAGATTGTCTTGTGCTGAAAGCGAAAGTACAATGTCAACATCAACACAG	302						
QY	250	ctcaactccagagagagaggaagtaattgtttccctgaaatggatggactcatttgttgc	309						
DB	303	CTCACTCCAGAGGAGGAGGAGTAATTGTTTCCCTGGAATGGGATGGACTCATITGTTGC	362						
QY	310	ccagaggaacagtggggaaatatcggtgttccatgcctcctcttattatgactca	369						
DB	363	CCAGAGGAACACTGGGAAAAATATCGGCTGTCCATGCCCTCCTTATATTTATGACTCA	422						
QY	370	accataaagaggttcttccgacactgtaaccccaatagaacatgggatttatgcaca	429						
DB	423	ACCATAAAGGAGTTGCTTTCCGACACTGTAAACCCCAATGGGATTTTATGCACA	482						
QY	430	gcttaataaaacatgggccaattattcagactgccttcgcttctgcagcagatata	489						
DB	483	GCTTAATAAAACATGGGCCAATTATTACAGACTGCTTCGCTTTGACAGCAGATATCA	542						
QY	490	gcataaggaagcaagaattctgtgaacgcctctatgtaatatataccgttggtactcca	549						
DB	543	GCATAGGAAAGCAAGAAATCTTTTGAACGCCTCTATGTAATGTATACCGTTGCTACTCCA	602						
QY	550	tctcttttggttccgttggtggttctctcatcatattggttacttcagacagattgcat	609						
DB	603	TCTCTTTTGGTTTCCCTTGGGCTGTGGCTATTCTCATCATTTGTTACTTCAGACCATTC	662						
QY	610	gcactaggaactatatccacatgcacttatttcttctctctgcgtgagactcaagca	669						
DB	663	GCACATAGGAACATATATCCACATGCACCTATTATTGTGTCTTTCATGCTGAGAGCTAC	722						
QY	670	tctttgtcaaacagacagagtagtccatgctcacataggagtaagagagctgggtccctaa	729						
DB	723	TCTTTTCTAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGTGGAGTCCCTAA	782						
QY	730	taatgcagatgacccacacaaaaattccattgagggcaactctctgtgacaaaatacaca	789						
DB	783	TAATGCAGGATGACCCACAAAAATTCATTGGAGCAACTTCTCTGGGCAAAATCACAA	842						

Db	1922	TTTTAGGTCATGAATTTGGCTCTGTAAATACTACGACATGAAAATCCAATGTCAATG	1981
Qy	1929	gagttagttattacacctcttatggcatcaagtttccctctcaaatcaatgtagtattctg	1988
Db	1982	GAGTACTTTATTTACCTTCTTATTTGGCATCAAGTTTTCCCTCAAAATTAATGTATGGTATTG	2041
Qy	1989	ctctgtgattgttca	2003
Db	2042	CTCTGTGATTGTCA	2056

LOCUS	G26909	2641 bp	DNA	STS
DEFINITION	human STS SHGC-31599,		sequence tagged site.	

14-JUN-1996

REFERENCE
AUTHORS
JOURNAL
Unpublished (1995)
Myers, R.M.
1 (bases 1 to 2641)
Mammals: Eutheria; Primates; Catarrhini; Hominoidea.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea.

Contact: Richard M. Myers

Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: AGGCTTGGCTGATACTCCT
Primer B: AGAAAAAATGAACAATCACAGAGC
STS size: 217
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation:	94 degrees C for 15 seconds
Annealing:	62 degrees C for 23 seconds
Polymerization:	72 degrees C for 30 seconds

Thermal Cycler: Perkin Elmer 9600

Template: 25 ng
Primer: each 1 μ M
dNTPs: each 200 μ M
Taq Polymerase: 0.05 units/ μ l
Total Vol: 10 μ l

Buffer:

MgCl₂: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from U25.128
 -- Washington University/Merck EST sequence.

[illegible]

	1849.	1865
STS	1849.	1865
primer bind	1849.	1868

primer bind complement(2041..2065)

BASE COUNT	670 a	564 c	623 g	784 t
ORIGIN				

Qy 1869 tttaggctccatgaattggctcctgtaaaatactaacgacatgaaaaatgcaagtgtcaatg 1928

Query Match				97.0%;	Score	1942.2;	DB	93;	Length	2641;					
Best Local Similarity				99.0%;	Pred.	No.	0;								
Matches				1975;	Conservative	0;	Mismatches	18;	Indels	2;					
						Gaps		2;							
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Qy	130	taatgctgcagctgcctccctggccagagccagctggattctgatggaccatacta	189												
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Qy	370	accataaaggagttgtcttccagactgtaaccccaatggaaacatgggattttatgcaca	429												
Db	423	ACCATAAAGGAGTGTGTTTCCGACACTGTAAACCCCAATGGAACATGGGATTTTATGCA	482												
Qy	430	gcttaataaaacatgggccaattatccagactgcttgcgtcttctgcagccagatatca	489												
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Db	723	TCCTTTGTCAAGACACAGTAGTCCATGCTTCACATAGGAGTAAAGGAGCTGGAGTCCC	782												
Qy	730	taatgcagatgacccacaaaattccattgaggaacactctgtggacaaatacaacata	789												
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Qy	850	tcctgggtgaaaggtctctacctgcataatctcatcttltgtggcttctcttccggacacca	909												
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Qy	910	aatacctgtggggcttca tcttgataggctgggggtttccacagcagcatttgttcagcat	969												
Db	963	AATACCTGTGGGGCTTCATCTTTGATAGGCTGGGGGTTCACAGCAGCATTTGTTTCAGCAT	1022												
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RESULT 3

RNU55836

LOCUS

DEFINITION

Rattus norvegicus parathyroid hormone receptor PTH2 mRNA, complete cds.

19-OCT-1996

ROD

mRNA

1977 bp

2056

2003

2056


```
QY 1562 ttacctggctatgtctggagtaactcagcagcaggagctgctcacacactctctccacag 1621
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Db 1682 CTACCTGGCTAGCTCGAGTAGTCTGAGCAGGAGCTGCAACCAACAATCTACCCGGAG 1741
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QY 1622 gagcaacaaggagaagtagtggaggcagagagatgatattctaatggagaagccttccag 1681
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Db 1742 GAG-CTATAAAGAGTCATGGCGCAGCAGCAAGATGATAGTCCAGTGGGGAGTCTTCCAG 1800
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RESULT 4
LOCUS HSPTHR05 1980 bp DNA PRI 21-OCT-1996
DEFINITION Human parathyroid hormone receptor (PTHR2) gene, exon 13 and
partial cds.
ACCESSION U47129
VERSION U47129.1 GI:1256371
KEYWORDS 5 of 5
SEGMENT human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1980)
AUTHORS Usdin,T.B., Gruber,C. and Bonner,T.I.
TITLE Identification and functional expression of a receptor selectively
recognizing parathyroid hormone, the PTH2 receptor
J. Biol. Chem. 270 (26), 15455-15458 (1995)
95318121
JOURNAL 2 (bases 1 to 1980)
MEDLINE Usdin,T.B., Modi,W. and Bonner,T.I.
REFERENCE Assignment of the human PTH2 receptor gene (PTHR2) to chromosome
2q33 by fluorescence in situ hybridization
Genomics 37 (1), 140-141 (1996)
97079671
JOURNAL 3 (bases 1 to 1980)
MEDLINE Bonner,T.I. and Usdin,T.B.
REFERENCE Direct Submission
AUTHORS
TITLE Submitted (25-JAN-1996) Tom I. Bonner, Lab of Cell Biology, NIMH,
Bldg. 36, Rm 3A17, MSC 4090, Bethesda, MD 20892-4090, USA
JOURNAL Location/Qualifiers
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/note="total approx. 2.4 kb"
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/number=13
polyA_site 1969
BASE COUNT 526 a 394 c 437 g 620 t 3 others
ORIGIN
Query Match 31.0%; Score 620; DB 91; Length 1980;
Best Local Similarity 98.2%; Pred. No. 4.7e-167;
Matches 648; Conservative 0; Mismatches 16; Indels 2; Gaps 2;
QY 1345 aggttcagcagagtggaagaagatgtgagtcggtgggaatctctccgtggactggaata 1404
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Db 725 AGGTTCAGGCACAGGTGAAGAAGATGTGGAGTCGGTGGAAACCTCTCCGTGGACTGAAAA 784
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QY 1405 ggacaccccatgtggcagccagatcggtcagtcagtcagtcacacccctgacgcacagca 1464
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Db 785 GGACACCCCCATGTGGCAGCCAGATGGGCTCAGTGCCTACACCCCTGACGCACAGCA 844
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QY 1465 ccagcagccagtccacaggtggcgg-cagcacacgcagtcggtcttatctctgcgaagctg 1523
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Db 845 CCAGCAGCCAGTCACAGTGGCGGCAGCACACGATGGTGTATCTCTGCAAAAGCTG 904
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QY 1524 ccaagatcgccagcagcagcctgacagccacatcaccttacctggctatgtctggagta 1583
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Db 905 CCAAGATGCCAGCAGCAGACAGCCTGACAGCCACATCACTTTACCTGGCTATGTC15GAGTA 964
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QY 1584 actcagcagagactgcctcacacactctctccacagagagcaacaagaagaatagtgag 1643
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Db 965 ACTCAGCAGCAGACTGCCTGCCACACTCTTTCCACAGAGAG-ACCAAGCAGAGATAGTGGG 1023
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QY 1644 aggcagagagatgatattctaatggagaagcctccagcctatggaatccttaaccagac 1703
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Db 1024 AGGCAGGAGATGATATCTTAATGGAGAGAGCCTTCAGGCCCTATGGAATCTAACCCAGAC 1083
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QY 1704 actgaagatgacaaggagaaactgagatgttctctgaatggacatgtgtggctgacct 1763
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QY 1944 ttctattggcatcaagtttccctctctctctctctctctctctctctctctctctctct 2003
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Db 1324 TTCTATTGGCATCAAGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1383
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RESULT 5
AC010822/c
LOCUS Homo sapiens clone RP11-3M22, WORKING DRAFT SEQUENCE, 13 unordered
pieces.
DEFINITION AC010822
ACCESSION AC010822
VERSION AC010822.4 GI:7341833
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 159700)
Birren, B., Linton, L., Nusbaum, C., and Lander, E.
Homo sapiens, clone RP11-3M22
Unpublished
2 (bases 1 to 159700)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE
JOURNAL

Submitted (23-SEP-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 30, 2000 this sequence version replaced gi:6454017.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

COMMENT

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2778
Center clone name: 3.M.22
----- Summary Statistics
Sequencing vector: M13; W77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145599 bases at least Q40
Consensus quality: 151691 bases at least Q30
Consensus quality: 154613 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 158500; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

* 1 1067: contig of 1067 bp in length
* 1068 1167: gap of 100 bp
* 1168 5145: contig of 3978 bp in length
* 5146 5245: gap of 100 bp
* 5246 11674: contig of 6429 bp in length
* 11675 11774: gap of 100 bp
* 11775 16018: contig of 4244 bp in length
* 16019 16118: gap of 100 bp
* 16119 22143: contig of 6025 bp in length
* 22144 22433: gap of 100 bp
* 22444 29636: contig of 7393 bp in length
* 29637 29736: gap of 100 bp
* 29737 37603: contig of 7867 bp in length
* 37604 37703: gap of 100 bp
* 37704 47116: contig of 9413 bp in length
* 47117 47216: gap of 100 bp
* 47217 61066: contig of 13850 bp in length
* 61067 61166: gap of 100 bp

* 61167 80698: contig of 19532 bp in length
* 80699 80798: gap of 100 bp
* 80799 103166: contig of 22368 bp in length
* 103167 103266: gap of 100 bp
* 103267 129867: contig of 26601 bp in length
* 129868 129967: gap of 100 bp
* 129968 159700: contig of 29733 bp in length.

FEATURES
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/db_xref="taxon:9606"
/clone="RP11-3M22"
/clone_lib="RPC1-11 Human Male BAC"

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1168. 5145
/note="assembly_fragment"
5246. 11674
/note="assembly_fragment"
11775. 16018
/note="assembly_fragment"
16119. 22143
/note="assembly_fragment"
22444. 29636
/note="assembly_fragment"
29737. 37603
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vector_side:left

misc_feature

37704. 47116
/note="assembly_fragment"
clone_end:T7
vector_side:right

misc_feature

47217. 61066
/note="assembly_fragment"
61167. 80698
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misc_feature

80799. 103166
/note="assembly_fragment"
103267. 129867
/note="assembly_fragment"

misc_feature

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BASE COUNT 50230 a 29925 c 30059 g 48284 t 1202 others
ORIGIN

Query Match 31.0%; Score 620; DB 39; Length 159700;
Best Local Similarity 98.2%; Pred. No. 9.5e-167;
Matches 648; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
QY 1345 aggttcaggcagaggtgaagaagatgtggagtcggtggaatctctcgtgagctggaata 1404
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Db 41949 AGGTTACGAGGAGGTGAAGAAGATGGAGTGGGACCTCTCCGTGGACTGGAAAA 41890
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Db 41889 GGACACCCCATGTGGCAGCGCGAGATGCGGCTCAGTGTCTACCCACCGTACGACGCA 41830
QY 1465 ccagcagccagtcacaggtggcgg-cagcacagcagtcggtgcttatctctgcaaaagctg 1523
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Db 41769 CCAAGATCGCCAGCAGACAGCCTGACAGCCACATCATCTTTACCTGGTATGTCTGGAGTA 41710
QY 1584 actcagcagcagcagcctcctcacacactctctccacgagcagcaacaggaagtagtggg 1643
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Db 41709 ACTCAGAGCAGGACTGCTGCCACACTCTTTCCACAGGAGGAG-ACCAAGGAAGATAGTGGG 41651
QY 1644 aggcagagagatgatatttctaattgagaagccttccaggcctatggaatcaccacagac 1703
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Db 41650 AGCGAGGAGATGATATCTTAATGGAGAGCCCTCCAGGCCCTATGGAATCTAACCCAGAC 41591

QY 1704 actgaaggtgacagagagaactgaagatgtctctgaatgacacatgtgtgctgaactt 1763

Db 41590 ACTGAAGGATGCCAGGAGAACTGAGGATGTCTCTGAATGACATTTGTGGCTGACTT 41531

QY 1764 tcatggctgggtccaatggctggtgtgtgtgagagggcttggctgatacctctatgcttga 1823

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QY 1824 gcacaaagctgaaataattcagtttaaggtgttacttaataatagtttttaggtccatgaa 1883

Db 41470 GTTCAAAGCTGAAATTCAGTTAAGGTGTACTTAAATAATAGTTTAAAGGCTCCATGAA 41411

QY 1884 ttggccctctgtaataactaacacatgaaatgcaagtgtcaatgagtagttattacc 1943

Db 41410 TTGGCTCCCTGTTAAATACCAACATGAAATGCAAGGTGCAATGGAGTAGTTTATACC 41351

QY 1944 ttctattggcatcaagtttctctctaaataatgtatgtatgttctctgtgattgttca 2003

Db 41350 TTCTATTGCGCATCAAGTTTCTCTCTAAATTAATGATGATGTTGCTCTGTGATTGTTC 41291

RESULT 6

AC019185 173316 bp DNA HTG 16-JUL-2000

LOCUS Homo sapiens chromosome 2 clone RP11-299P7, WORKING DRAFT SEQUENCE, 9 unordered pieces.

ACCESSION AC019185

VERSION AC019185.6 GI:9211380

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 173316)

AUTHORS Waterston,R.H.

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 173316)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Jul 15, 2000 this sequence version replaced gi:8980958.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----

Center project name: H_NH0299P07

----- Summary Statistics -----

Sequencing vector: pML3; %

Chemistry: Dye-primer ET; % of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 169101 bases at least Q40

Consensus quality: 170008 bases at least Q30

Consensus quality: 170805 bases at least Q20

Insert size: 164000; agarose-fp

Insert size: 172516; sum-of-contigs

Quality coverage: 5.71 in Q20 bases; agarose-fp

Quality coverage: 6.25 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

* as soon as it is available and the accession number will be preserved.

1 1606: contig of 1606 bp in length

1607: gap of unknown length

1707 3626: contig of 1920 bp in length

3627: gap of unknown length

3727 7755: contig of 4029 bp in length

7756: gap of unknown length

7841: contig of 9986 bp in length

17842 30924: contig of 12983 bp in length

30925 31024: gap of unknown length

31025 46299: contig of 15275 bp in length

46300 46399: gap of unknown length

46400 71861: contig of 25462 bp in length

71862 71961: gap of unknown length

71962 119567: contig of 47606 bp in length

119568 173316: contig of 53649 bp in length.

119668 173316: contig of 53649 bp in length.

FEATURES

Location/Qualifiers

1..173316

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db_xref="taxon:9606"

chromosome="2"

clone="RP11-299P7"

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vector_side:left"

BASE COUNT 54299 a 32790 c 32650 g 52776 t 801 others

ORIGIN

Query Match 31.0%; Score 620; DB 43; Length 173316;

Best Local Similarity 98.2%; Pred. No. 9.7e-167;

Matches 648; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 1345 aggttcacgacaggtggaagaagatgtgagtcggtgggaatctctccgtgactggaaaa 1404

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Db 154747 AGGTTACGACAGGTGACAGAGATGTGAGTCGGTGGAGACCTCTCCGTGGACTCGAAAA 154806

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QY 1405 ggacaccgccatgtggcagcccgacagtcggtctcagtcagtcaccaccgltgacgcacacga 1464

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Db 154807 GGACACCGCATGTGGCAGCCGACAGATGGGCTCAGTGTCTACCCCGTGACGCACAGCA 154866

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QY 1465 ccagcagccagtcacaggtggcggc-cagcacacgcatggtgcttatctctgcaagctg 1523

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QY 1524 ccaagatcccgacagacagcctgacagccacatcacttacctgctatgctgagta 1583

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Db 154927 CCAAGATCCCGACAGACAGACCTTGACAGCCACATCATTACTTACCTGGCTATGCTGGAGTA 154986

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Db 155226 GTTCAAAAGGCTGAAATTCAGTTAAGGTGTTACTTAATAATAGTTTTTAGCTCCATGAA 155285
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AF132082 2429 bp mRNA VRT 29-OCT-1999
LOCUS Danio rerio parathyroid hormone type-2 receptor precursor, mRNA,
DEFINITION complete cds.
ACCESSION AF132082
VERSION AF132082.1 GI:5805256
KEYWORDS zebrafish.
SOURCE
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasbora; Danio.
REFERENCE 1 (bases 1 to 2429)
AUTHORS Rubin,D.A., Hellman,P., Zon,L.I., Lobb,C.J., Bergwitz,C. and Juppner,H.
TITLE A G protein-coupled receptor from zebrafish is activated by human parathyroid hormone and not by human or teleost parathyroid hormone-related peptide. Implications for the evolutionary conservation of calcium-regulating peptide hormones
J. Biol. Chem. 274 (33), 23035-23042 (1999)
J9367425
2 (bases 1 to 2429)
AUTHORS Rubin,D.A., Hellman,P., Zon,L.I., Lobb,C.J., Bergwitz,C. and Juppner,H.
TITLE Direct Submission
SUBMITTED (01-MAR-1999) Endocrine Unit, Wellman 5, Massachusetts General Hospital, Fruit Street, Boston, MA 02114, USA
FEATURES
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/db_xref="taxon:7955"
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103. .1830
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BASE COUNT 634 a 555 c 580 g 660 t
ORIGIN
Query Match 29.7%; Score 594.4; DB 4; Length 2429;
Best Local Similarity 64.6%; Pred. No. 1.le-159;
Matches 977; Conservative 0; Mismatches 506; Indels 29; Gaps 5;
Qy 174 gatggaccatacactatagagagagatgtctctgtctgtaagcgaaagtaacaatgt 233
Db 280 GATGGCAGATTACAGCTGAAGAACAGCATCAAAATGCTGCTGGATGCAAGCTGCAGTGC 339
Qy 234 gaactcaacatcacagctcaactccagagaggaagaagtaattgttccctgaatggat 293
Db 340 CTCCAAAAGGTTCTCCAGCGATGACC---CTGCAAGTTGGTGTGTGTGCCAGAGTGGAT 396
Qy 294 ggaactcatttggccccagaggaacagtggggaaaaatctcggtgttccatgcccctct 353
Db 397 GGTCTGATATGTTGCCACAAAGGTTCTCTGGGAGGCTGACCAAGACACCTGCCCTGGA 456
Qy 354 tatatttatgactccaaccataaaggaggtgtcttctcogacactgtaaccccaatggaaca 413
Db 457 TACATCTATGACTTCAACCATGCAGCATGCATACAGAGGTTGTGACTCTAATGGTTCC 516
Qy 414 tgggaatttatgcagacttaataaaaaatcattggcccaattattcagactgctctgcttt 473
Db 517 TCGGTGCTGGCAGAGAGCTCAACAAGACCTGGGTCAACTACACTGAATGATCAAAAT-- 574
Qy 474 ctgcagccagatatcagcataggaagcaagaattctgtgaacgacctctatgtaatgtat 533
Db 575 ----CCCCAGAGCCCAACAAAAGACAGAGCTCTTTTGAACGGCTGCACATCATGTATC 630
Qy 534 accdttggctactccatcttctgttctgttctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 593
Db 631 ACAGTCGGCTATGAGTGTCTTCTTTCAGCTCTCTCTAGTGGCCATCTTTATTATCGGATAT 690
Qy 594 ttcagagatttgattgcaactaggaactatatacactgacacttatttcttcttcttctatg 653
Db 691 TTCAGAGACACTCCACTGCACCAGGAACATACATTCACATGCACCTGTGTTGTTTCTTTATG 750
Qy 654 ctgagagctacaagcatcttctcaaaagacagatgagtcctcatcactcagaggaagaaag 713
Db 751 CTGGTCCGCCACAGATCTTTGTGAGGATCAGTGTGTGACACTAGCGCCGGCTGCAG 810
Qy 714 gagctggagtcctcctaataatcagagatgaccccaaaaattccattgagggcaactctgtg 773
Db 811 GAATCTGATGCTGTGCTCAT---GAATAACTTACCAATGCTGTGGATGTGACACCATGTG 867
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RESULT 14

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 LOCUS RATPATHYR 2065 bp mRNA ROD 27-APR-1993
 DEFINITION Rat parathyroid hormone receptor mRNA, complete cds.
 ACCESSION M77184
 VERSION M77184.1 GI:206034
 KEYWORDS parathyroid hormone receptor; parathyroid hormone-related receptor; transmembrane glycoprotein.
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 2065)
 AUTHORS Abou-Samra,A.-B., Jueppner,H., Force,T., Freeman,M.W., Kong,X.-F., Schipani,E., Urena,P., Richards,J., Bonventre,J.V.,

Potts,J.T., Kronenberg,H.M. and Segre,G.V.
 Expression cloning of a common receptor for parathyroid hormone and parathyroid hormone related peptide from rat osteoblast-like cells: A single receptor stimulates intracellular accumulation of both cAMP and inositol trisphosphates and increases
 Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736 (1992)
 92212903
 Complete title:
 Expression cloning of a common receptor for parathyroid hormone and parathyroid hormone-related peptide from rat osteoblast-like cells: A single receptor stimulates intracellular accumulation of both cAMP and inositol trisphosphates and increases intracellular free calcium.

FEATURES

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RESULT 15
MMPHRP M. musculus mRNA for parathyroid hormone/parathyroid hormone related peptide receptor. ROD 04-MAY-1994
LOCUS M.musculus mRNA for parathyroid hormone/parathyroid hormone related peptide receptor. X78936
DEFINITION G-protein coupled receptor; parathyroid hormone; parathyroid hormone related peptide receptor; parathyroid hormone-related peptide; parathyroid hormone-related protein.
ACCESSION X78936
VERSION 1
KEYWORDS G-protein coupled receptor; parathyroid hormone; parathyroid hormone related peptide receptor; parathyroid hormone-related peptide; parathyroid hormone-related protein.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1984)
AUTHORS Karperien, M., Van Dijk, T.B., Hoeljmakers, T., Cremers, F., Abou-Samra, A.B., Boonstra, J., De Laat, S.W., and Defize, L.H.K.
TITLE Expression pattern of parathyroid hormone/parathyroid hormone

related peptide receptor mRNA in mouse postimplantation embryos indicates involvement in multiple developmental processes
Unpublished
2 (bases 1 to 1984)
AUTHORS Karperien, M.
DIRECT SUBMISSION
JOURNAL TITLE
JOURNAL
FEATURES
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PF 05-JUN-1995; 95WO-US07085.
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PR 05-JUN-1995; 95WO-US07085.
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XX (HUMA-) HUMAN GENOME SCI INC.
PA
PI Li Y, Rosen CA, Ruben SM, Soppet DR;
XX
XX WPI: 1997-043068/04.
DR P-PSDB; W12695.
XX
XX Human G-protein parathyroid hormone receptor, HLTDC74 - used to
PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
XX
XX Claim 1; Fig 1A-E; 62pp; English.
XX
CC A cDNA clone (T59619) codes for a 7-transmembrane receptor (W12695)
CC which has been identified as a human G-protein parathyroid hormone
CC (PTH) receptor, designated HLTDC74. It was isolated from a human T
CC cell lymphoma tissue cDNA library. The cDNA can be utilised in the
CC prodn. of recombinant HLTDC74 and to design probes e.g. to detect
CC mutations in the receptor gene. Gene therapy methods can be used to
CC treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism and
CC chronic tetany by stimulating an increase in serum calcium levels.
CC Antisense constructs can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphataemia, kidney stone, nephroliasis.
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RESULT 4

Q29605
 ID Q29605 standard; cDNA; 1863 BP.

XX AC Q29605;

XX DT 16-MAR-1993 (first entry)

XX DE Opossum kidney PTH/PTHrP receptor clone, OK-O.

XX KW Parathyroid hormone; related protein; calcium; antagonist;

XX KW antibodies; hypercalcaemia; ss.

XX OS Didelphis virginiana.

XX FH Key Location/Qualifiers
 XX FT CDS 98..1855
 XX FT /*tag= a

XX PN W09217602-A.

XX PD 15-OCT-1992.

XX PF 06-APR-1992; 92WO-US02821.

XX PR 05-APR-1991; 91US-0681702.

XX PR 06-APR-1992; 92US-0864475.

XX PA (GRHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
 XX PI Segre GV;

XX DR WPI; 1992-366271/44.

XX DR P-PSDB; R27705.

XX PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
 XX PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 XX PT and treatment of tumours

XX PS Disclosure; Fig 2; 91pp; English.

XX CC Total RNA was isolated from opossum kidney (OK) cells and used to
 CC prep. a cDNA library. The resultant phage libraries were used to
 CC transform E. coli contg. a larger helper plasmid p3. The cells were
 CC screened to isolate those expressing functionally intact OK cell
 CC parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
 CC receptor proteins, performed according to Gearing et al., (EMBO J.
 CC 8: 3676, 1989), by identifying colonies capable of binding a
 CC suitable radiolabelled ligand. The clone OK-O is identical to the
 CC OK-H clone except at the C-terminal tail as OK-O encodes a 585 amino
 CC acid protein, OK-H encodes one of 515 amino acids. The difference is
 CC attributed to a single nucleotide deleted in the OK-H sequence causing
 CC a frame shift and an earlier stop codon. It is not known whether OK-O
 CC and OK-H represent prods. of two separate genes or are a laboratory
 CC artifact. The clone encodes a protein which may be used in a
 CC therapeutic compsn. to inhibit activation of PTH or PTHrP and thus

CC reduce the level of calcium in the blood. Cpd. capable of competing
 CC with PTH or PTHrP for binding can be identified using the protein prod.
 CC and DNAs homologous to PTH DNA can be identified using fragments of the
 CC clone as probes. The sequence may be used for the prodn. of antibodies
 CC useful for the treatment, classification, prognosis and/or treatment of
 CC disorders related to the interaction between a cell receptor and a
 CC ligand such as in hypercalcaemia. See also Q29604-11.
 XX

SQ Sequence 1863 BP; 411 A; 494 C; 518 G; 440 T; 0 other;

Query Match 22.6%; Score 452.6; DB 13; Length 1863;
 Best Local Similarity 63.0%; Pred. No. 1.7e-134;
 Matches 752; Conservative 0; Mismatches 429; Indels 12; Gaps 3;

Qy 257 ccaggaggaggaaggttaattttccctgaatggatggatgactcatttttgccagagg 316
 Db 391 ccggctcaggatggctctccctacctgagtggaacacattgtgctggcctgctgg 450
 Qy 317 aacagtggggaaaatattcgctgttcccatgccctccctatatattatgactcaacataa 376
 Db 451 agtgcgcgcgaagtggtggcgtgcccgtcccgactactctacgactcaaccacaa 510
 Qy 377 aggagtgcttccgacactgaaccccaatggaaacatgggattttatgcacagcttaa 436
 Db 511 aggcgcagcctatcgcgctgtgacagcaatggcagctgggagctggctgggaacaa 570
 Qy 437 taaacatgggccaattattcagactgccttcgctcttctgcagccagatatacagcatagg 496
 Db 571 ccggatcggcggaattacaggaatgttcaagttttctgccaacagagacc-----cg 624
 Qy 497 aaagcaagaattctggaacgcctctatgtatgtataccgttggtactccatctctt 556
 Db 625 ggaacgggaagtctttgatgcctcgcgaatgatctacactgggctattccatctctct 684
 Qy 557 tggttccttggtggtctattctcatcattggttacttcagacgattgcatcactag 616
 Db 685 gggtctcctcactgtgctgtcgatctctgggttaactttaggaggttacattgcaccgc 744
 Qy 617 gaactatatacagatgcacttattgtgtcttcttcagctgagagacatacatctttgt 676
 Db 745 aaactacattccatgcatctctctcgtctcttcttgcctcgttgcctgggttaagcatctctat 804
 Qy 677 caagacagagatgtccatgctccatagagagtaaaagagctggaagtcctccataaataatga 736
 Db 805 caaggtgctgctctactcctcgggggtttccacagatgaataatcgag---cgcataccaga 861
 Qy 737 ggatgacccacaaaattccattgaggcaactctctgtggacaaaatcacataataatcggtg 796
 Db 862 ggaggagctgaggcccttcacagagccctccctcgtcgacaaaggcgggttttgggctg 921
 Qy 797 caagattgctgtgtgatttattactcctcctggctacaaaattattattgagctcgtgt 856
 Db 922 cagatgtaggtaaacctctctcttactcctgaccaccactactactgagctcgtgt 981
 Qy 857 ggaaggtctctacctgcataatactcattctgtgctttcttttcggacacaaataacct 916
 Db 982 ggaaggcctcactctcacagcctcattctcattggtcttctctctgagaaaagtatct 1041
 Qy 917 gtgggcttctcattgataggctgggggtttcccgagcagcattttgtgcagatggcgtgt 976
 Db 1042 ctggggttcacattatttgctggggcctccctgcgcgtgtttgcgtgtgtgggtgac 1101
 Qy 977 ggcacgagcaactcgtcgtgtagcaggtgctgggaactgtagtgcgtggagacataagtg 1036
 Db 1102 cgtgaggtctacatcgtgccaacactgagtgctgggacgtgagctcggggaataagaatg 1161
 Qy 1037 gatttatacagcagcagcttagcagctattggctgaattttattcttcttctgaatac 1096
 Db 1162 gatcatacaggtgcccattcctggtgagctattgtgtgaaacttattcttcttcaaatat 1221
 Qy 1097 ggttagagttctagctaccaaaatctggagaccaaataagcagttggcagatgacaaagaa 1156

Db 1402 gcactatgaatgctcttaattcattccaggagatttctcgttgccattatatactgttt 1461
QY 1334 ctgcaatggagaggttcacgacagaggtgaagaagatgtgagtcggtggaatctccggt 1393
Db 1462 ctgcaatggagaggtacacgacagagatcaagaagtcagtgaagccgtggaacctggcctt 1521
QY 1394 ggactggaagagacacccgccatgtggcagccgcagatcgggtcagtgctca 1446
Db 1522 ggactlcaagcgaagcccgagtgccagcagctacagctacagctagggcccca 1574

RESULT 7
Q29604
ID Q29604 standard; cDNA; 1862 BP.
AC Q29604;
XX
DT 16-MAR-1993 (first entry)
XX
XX Opossum kidney PTH/PTHrP receptor clone, OK-H.
XX
DE Parathyroid hormone; related protein; calcium; antagonist;
KW antibodies; hypercalcaemia; ss.
KW
XX
OS Didelphis virginiana.
XX
FH Key Location/Qualifiers
FT 98..1645
FT /*tag" a

XX W09217602-A.
XX 15-OCT-1992.
XX
XX 06-APR-1992; 92WO-US02821.
XX
XX 05-APR-1991; 91US-0681702.
PR 06-APR-1992; 92US-0864475.
XX
XX (GEHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
XX
XX Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;
XX
XX WPI: 1992-366271/44.
DR P-PSDB; R27704.
DR
XX
XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours
XX
XX Claim 2; Fig 1: 91pp; English.

XX
CC Total RNA was isolated from opossum kidney (OK) cells and used to
CC prep. a cDNA library. The resultant phage libraries were used to
CC transform E. coli contg. a larger helper plasmid p3. The cells were
CC screened to isolate those expressing functionally intact OK cell
CC parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC receptor proteins, performed according to Gearing et al., (EMBO J.
CC 8: 3676, 1989), by identifying colonies capable of binding a
CC suitable radiolabelled ligand. The clone encodes a protein which
CC may be used in a therapeutic compsn. to inhibit activation of PTH or
CC PTHrP and thus reduce the level of calcium in the blood. Cncls.
CC capable of competing with PTH or PTHrP for binding can be identified
CC using the protein prod. and DNAs homologous to PTH DNA can be
CC identified using fragments of the clone as probes. The sequence
CC may be used for the prodn. of antibodies useful for the treatment,
CC classification, prognosis and/or treatment of disorders related to
CC the interaction between a cell receptor and a ligand such as in
CC hypercalcaemia. See also Q29605-11.
XX
XX Sequence 1862 BP; 407 A; 497 C; 520 G; 438 T; 0 other;

Query Match 22.5%; Score 451; DB 13; Length 1862;
Best Local Similarity 63.0%; Pred. No. 5 4e-134;
Matches 751; Conservative 0; Mismatches 430; Indels 12; Gaps 3;
QY 257 ccaggaggagagaaggttaattgtttccctgaaatgggtaggactcatttgttggcccgagag 316
Db 391 ccggctgcagagtggtcttctgctaactgagtgggacaacattgtgtgctggcctgctgg 450
QY 317 aacagtgggaaaaatatcgctgttccatgcctctcttattattatgaactcaaccataa 376
Db 451 agtgcgccggcaaggtggtggtgcgtgcccgtgaccttctacgaactcaaccacaa 510
QY 377 aggagttgctttccgacactgtaaccccaatggaacatgggatttttatgcagacttaaa 436
Db 511 aggcgagcctatcggcgctgtgacagcaatggcagctggggagctggctcgggaacaa 570
QY 437 taaacatgggccaattattcagaactgccttcgctttctgcagccagatatcagcatagg 496
Db 571 ccggacatgggcgaattacagcgaatgtgtcaagtttctgaccaacagagacc-----cg 624
QY 497 aaagcaagaattctgtgaacgctctatgtaatgtatacogttggtactccatctcttt 556
Db 625 ggaacgggaagtctttgatcgcctcggaatgatctacactgtgggtactccatctctct 684
QY 557 tggttccttggctgtgctatttctcatcattggttacttcagacgattgcattgcactag 616
Db 685 gggctccctcactgtggctgtgctgattcttgggttactttagggaggttaccttgaccgg 744
QY 617 gaactatattccacatgcacttattgtgtctttctcatgctgagagctcacaagcatctttgt 676
Db 745 aaactacattcacatgcactctcttctgtcttattgtcccttgcctggctgtaagcatctcat 804
QY 677 caaagacagagtagtccatgctcaacataggaagtaagagctggagctccctataataatga 736
Db 805 caaggtgctgtgctactcgggggtttccacagatgaatcagag---cgatcaccca 861
QY 737 ggaatgacccacaaaattccatgaggaactctgtggacaatacacaatatatcgggtg 796
Db 862 ggaggagctgaggggcttcacagagcctccctcctgcgcagaggggggttttgtgggctg 921
QY 797 caagatgtgtgtgtgatgtttatttacttctcctggctggaacttagtctgggagacataagtg 856
Db 922 cagagtggcggtaaacgctcttcttacttctgaccacaaactactactgcatcctcgtt 981
QY 857 ggaaggtctctacctgcataatactcatttbggtcttcttcttgggacacacaaatacct 916
Db 982 ggaaggcctctaccttcacagcctcatcttcaggtttttctctctgagaaaaatctct 1041
QY 917 gtggggcttcatcttgataggtcgggggtttccagcagcatitgttgacagatgggctgt 976
Db 1042 ctgggggtttcacattatttggctggggcctccctcctgcgtgtgtgtcgtgtgtggatgac 1101
QY 977 ggcacgagcaactctcgtgtgatgcgaggtgtcgggaacttagtctgggagacatacaagtg 1036
Db 1102 cgtgagggtctacactggcccaacactgagtgctgggacctgagttcggggaaataagaaatg 1161
QY 1037 gatttatcaagcacccagatcttagcagctattgggctgaattttatctctgttctgaatac 1096
Db 1162 gatcatcagggtgccatctcgtgcagctattgtgtggaactttattctttttatcaatat 1221
QY 1097 ggttagagttcttagctacaaaattctggagaccactcagttgggcatgacacacaaggaa 1156
Db 1222 aatcagagtccttggctactaaactccgggagaccactcagggagagatgtgcacagggca 1281
QY 1157 gcaatacaggaactggccaaatcgacactggtctcctggttccttagtcttgggagtgattta 1216
Db 1282 acagtataaagcgtgtaagtcacgcgtagtctcctcagtcgctatttgggggtgcacta 1341
QY 1217 catcgtgttctgtgctcgtcctcactcct---tcactgggctcgggtgggagatccgcat 1273
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QY 1336 gcaatggagaggttcaggcagaggtgaagaagatgtggagtcggtggaatctctccgtgg 1395
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1457 gcaatggtaggtgcagcagagattaggaagtcaggagccgctggacacaggcgttgg 1516

QY 1396 actggaagggacacccgcatgtggcagccgagatgcggt 1437
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1517 acttcaagcgaagcacgaagtggagtagcagctacagct 1558

RESULT 9
V08390 ID V08390 standard; DNA; 2051 BP.
XX AC
XX V08390;
XX DT 08-FEB-1999 (first entry)
XX DE Parathyroid hormone receptor R15B coding sequence.
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
KW PTH-related hypercalcaemia; rat; ds.
XX OS Rattus sp.
XX FH Key
XX FT Location/Qualifiers
XX FT 73..1848
XX FT /*tag- a
XX PN US5840853-A.
XX PD 24-NOV-1998.
XX PF 06-JUN-1995; 95US-0471494.
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX PA (GEO ) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX WPI: 1999-034124/03.
XX DR P-PSDB; W73316.
XX PT Antibody to parathyroid hormone receptor - for diagnostic or
XX PT therapeutic use
XX PS Claim 6; Fig 3; 63pp; English.
XX CC This sequence encodes the rat parathyroid hormone (PTH) receptor
XX CC R15B, which is targeted by the antibody of the invention. The antibody
XX CC of the invention is immunoreactive with naturally occurring human, rat
XX CC opossum PTH receptor. The antibody is useful for treating disorders
XX CC characterised by overstimulation of PTH receptors by their ligand and for
XX CC the diagnosis of PTH-related hypercalcaemia.
XX SQ Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 other;

Query Match 22.2%; Score 445.2; DB 20; Length 2051;
Best Local Similarity 62.9%; Pred. No. 4.2e-132;
Matches 744; Conservative 0; Mismatches 423; Indels 15; Gaps 3;

QY 265 ggaaggtgaattgttcctcgtgaatggatggactcattgttgcccgaggaacaagtgg 324
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 gagggcgctccctgtctgcccgagtgggaacaacatcgtttgtgcccattaggggcaccag 442

QY 325 ggaataatcggctgttcacatgccctcctattattatgacttcaaccaataaagagtgg 384
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 gtgaagtggtgcagtagcttgcgcgattacattattgacttcaatcacaaagggcctg 502
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QY 385 ctttcgcagactgtaaccccaatggaaacatgggattttatgcacagcttaataaaaaacat 444
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Db 503 cctacagacgctgtaccgcaatggcagctggagtggttccagggcacaacccgagcgt 562

QY 445 gggcaattattcagacgctcttcgtcttcttcgacgcccagatatcagcatagaaagcaag 504
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 563 gggcaactacagcgagtgctcctaagttcatgacaaatga-----gacgcgggaacggg 616

QY 505 aattctgtgaacgcctctatgtaatgtataacgcttggctactccactctcttltgttct 564
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Db 617 aggtatttgacgcgcctaggcatgatacacgcgtggatactccatgtctcgcctccc 676

QY 565 tggctgtggctattctcatcattggttacttcagacgattgcattgcactcaggaactata 624
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Db 677 tcacggtggctgtgctcatcctggcctattttagcgcgctgcactgcacgcgcaactaca 736

QY 625 tcacatgcacttatttgtcttcttcactgctgagagctacaagcatctttgttcaagaca 684
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Db 737 tcacatgcacatgttctcgtctgtttatgtcgcgcgcgagcatcttcgtgaaggacg 796

QY 685 gagtagtccatgctcacataggagtaaaaggagctggagctccctataataatgcaggatgacc 744
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Db 797 ctgtgctctactctgtctcagcctggatggatggcgcgagcgcctcacagagggaaggtgc 856

QY 745 cacaaaattccattgagcgaactctgttgacaaaatc-----acaaatatatcggtgca 798
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Db 857 acatcatgcgcaggtgcccacctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 916

QY 799 agattgctgtgtgatgtttattactctcctggctacaaaattattattggatcctcgttgg 858
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Db 917 gcgtggcggtgacctctctactctactctcctggctaccaaactactactggtattcgttgg 976

QY 859 aaggctctacactgataataatctcatcttctgtggtcttcttcttcggacaccaaataacctgt 918
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QY 919 ggggcttcactgtgataggctgggggttccacgacgacattttgtcagcatggcctgttgg 978
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Db 1097 tcagagcaacctggcccaacactgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1156

QY 1039 ttatcaagcacccgatcttagcagctattgggctgaaattttattcttcttctgaatacgg 1098
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Db 1157 tcatccaggtgcccatcctggtcatctgtgtgtcctcaactctatctcttttatacaacatca 1216

QY 1099 tttagagttctagtaccaaaatctgggagaccaatgacattggtggtgcatgacacaagaagc 1158
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1217 tccgggtgcttgccactaagcttcgggagaccaatgctgggcccgtgtgacacccagcagc 1276

QY 1159 aatacaggaactctggcaaatcgacactggtcctgtcctgtctgtctgtctgtgtgtgtgtgtgt 1218
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1277 agtaccgaagctgctcaggtccacgctgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1336

QY 1219 tcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1275
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1337 ccgttctcatggccttgccgtacacccaggtctcaggggacattgtggcagatccagatgc 1396

QY 1276 actgtgagctctcttcaactccttccaggtttcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1335
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Db 1397 atatagagatgctctcaactcctccagggatttttctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1456

QY 1336 gcaatggagaggttcaggcagaggtgaagaagatgtggagtcggtggaatcctcctcgtgg 1395
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Db 1457 gcaatggtaggtgcaggcagagattaggaagtcatgagcgcgtggacacatggcgttgg 1516

QY 1396 actggaagggacacccgcctatgtggcagccgcagatgcggct 1437
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Db 1517 acttcaagcgaagcacgaagtggagtagcagctacagct 1558
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[illegible]

Query Match	7.8%;	Score 156.2;	DB 16;	Length 1377;
Best Local Similarity	56.4%;	Prod. No. 1.6e-39;		
Matches 337;	Conservative 0;	Mismatches 248;	Indels 12;	Gaps 2;

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QY	850	tcttgggtggaaggtctctacctgcataatctcatcttcttgctcttctttctcgacacca	909
Db	701	tgcttggtggagggcctctacctgcacacctacttcgcgtgctcttctctctgagcgga	760
QY	910	aatacctgtggggcctcatctttagctggggggtttccagcagcattttgttcagcat	969
Db	761	agtaactctgggtacatatcttcgtgggggtgcccagcaccttcacatgggtg	820
QY	970	ggcctgtggcagcagcaactctggctgatcgagaggtgctgggaaacttagtctctggagaca	1029
Db	821	ggaccctgcgcagaatccattttgagattatggatgctgggacaccaaccactctcac	880
QY	1030	tcaagtggattattcacagcaccgctcttagcagctattggctgaattttattctgtttc	1089
Db	881	tgtggtggatacataaaggccccatctctgcctccactcctgtggaactcactcattca	940
QY	1090	tgaatacgggttagagtcttagctaccaaaaactctgggagaccaatgcagttggggcatgaca	1149
Db	941	ttcgcatcatcgaaatcttggttcagaaactgcacccccagatgtcgggaagagtgaca	1000
QY	1150	caagggaagcaatcacaggaaactggccaaatcgacactggctcgtgctagtctttggag	1209

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Qy	1210	tgcaattacatcgtgttcgtgcctgcctcactcctcctcactcgggtcgggtgggagatcc	1269		
Db	1058	tgcaactacatcatgttgcctctcctcctgcacaatttaaagcc-----gaagtga	1108		
Qy	1270	gcattgcactgtgagctctctctcactcctctcactcctcttcagggtttcttgctcatcatctact	1329		
Db	1109	aaatggtcttgagctcactcgtgggatcttccagggttg-gtgggtggccatcctctact	1168		
Qy	1330	gctactgcacatggagaggttcagcagcagaggtgaaagaacatgtggaagtgcgtggaatc	1396		
Db	1169	gcttctcctaagtgtgaggtgcagcagcagctgcgcggaagtgcgcgcgtcgtggcacc	1225		
RESULT 15					
Q33018	Q33018 standard; DNA; 1794 BP.				
AC	Q33018;				
DT	28-APR-1993 (first entry)				
XX	Gene encoding the secretin receptor.				
DE	Rat; rat/mouse hybridoma; NG 108-15; over expressed; ss.				
KW	Rattus rattus.				
OS					
XX					
FH	Key	Location/Qualifiers			
FT	CDS	211..1560			
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FT		/*tag= c			
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FT		/*tag= d			
FT	primer_bind	1703..1723			
FT		/*tag= e			
FT		/note= "PCR primer binding site (3'-5')"			
FT		/note= "PCR primer binding site (5'-3')"			
XX	WO9221754-A.				
PN					
XX	10-DEC-1992.				
PD					
XX	05-JUN-1992;	92WO-JP00728.			
PF					
XX	07-JUN-1991;	91JP-0163946.			
PR					
XX	(OSAB-) OSAKA BIOSCIENCE INST.				
PA					
XX					
PI	Ishihara T, Nagata S, Takahashi K;				
XX					
DR	WPI: 1992-433652/52.				
DR	P-PSDB; R30187.				
XX					
PT	DNA coding for secretin receptor - is expressed in COS cells and produces a receptor protein for research and clinical use				
XX					
PS	Claim 1; Fig 1; 44pp; Japanese.				
XX					
CC	The DNA sequence encodes a secretin receptor of rat origin, contained in rat/mouse hybridoma NG108-15. The DNA sequence was obtd. from a cDNA library derived from NG108-15 cells. Expression in a suitable host allows prodn. of the receptor protein. The secretin receptor protein encoded by this gene may be used in basic research and in clinical tests, and is available in high yield.				
CC					
XX	Sequence 1794 BP; 390 A; 526 C; 471 G; 407 T; 0 other;				
SQ					

Query Match	7.38;	Score 145.4;	DB 13;	Length 1794;
Best Local Similarity	54.6;	Pred. No. 5.7e-36;		
Matches 365;	Conservative 0;	Mismatches 286;	Indels 18;	Gaps 3;
Qy 722	gtccctaataatgagatgacccacacaaaattccattgaggcaacttcgtggacaaatc	781		
Db				
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Db				
Qy 782	acaatatatcgggtgcagattgtgtgtgtgatgtttatttacttctcctgggtacaaatta	841		
Db				
Qy 840	ccataaagtcggctgcgaagctggctcatgatctctccagctactgcatcatggtccaaacta	899		
Db				
Qy 842	ttatggatcctggtggaagctctcactcgcataatactcaactcttctggtgtttcttttc	901		
Db				
Qy 900	cgcattgctgctggtggagggcctcactcacttcacacactcttgccactctcctctcttc	959		
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Qy 902	ggacccaatactctggtggcctcactctgataggctgggggtttccagcagcatttgt	961		
Db				
Qy 960	agaaaggaagcactctcagggcctctgtgctcctcggatgggggtctccagccatttttgt	1019		
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Qy 962	tgcagcatgggctgtggcagcagcaactctggctgatgctgcgaggtgctgggaacttagtgtc	1021		
Db				
Qy 1020	tgctttggtgctatcacacaggcactttctagaaaaactgagtgtggtggacatcaacgc	1079		
Db				
Qy 1022	---tggagacacaaagtggatlttatcaagcacccatcttagcagctatctggctgaaattt	1078		
Db				
Qy 1080	caatgtctcctgctgggtgcattcgaggcctgtgattctgctccactctgatacaattt	1139		
Db				
Qy 1079	tattctgtttctgaatacggcttagagttctagctaccaaaatctgggagaccaatgcagt	1138		
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Qy 1140	catctctctataaacttcaagaatcctgatagggaacttagaacacagaagaaacag	1199		
Db				
Qy 1139	tgggcatagcacaaaggaagcaatcaggaactggcgaactcgacactgtgctctggtcct	1198		
Db				
Qy 1200	aggaagtgaaca--aacattataagcgcctggccaagtccacctctcgtgataccc	1256		
Db				
Qy 1199	agctcttggagtgcatattacatcgtgttgctgctcactcactctcactgtggctcgg	1258		
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Qy 1257	gctctttggcatccactacattgtcttcgc-----cttctcccagaggagcgc	1304		
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Qy 1259	gtggagatccgatgcactgtgagctctcttcaactcctttcagggtttctttgtgtc	1318		
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Db				
Qy 1319	tatcatctactgctactgcatacggagaggttccaggcagaggtggaagagatgtgtagtcg	1378		
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Qy 1365	tgtcctttacgtctcctcaatgtgtgaggtgcagttggaagtgcagaaaaaatggcgcca	1424		
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Qy 1379	glgaatatct 1387			
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Qy 1425	gtggcacct 1433			
Db				

Search completed: November 15, 2000, 20:34:56
Job time: 3585 sec

us-09-236-468a-1.rni

Thu Nov 16 15:40:12 2000

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
November 15, 2000, 19:27:28 ; Search time 85.97 seconds
Run on: November 15, 2000, 19:27:28 ; (without alignments)
3523.748 Million cell updates/sec

Title: US-09-236-468A-1
Perfect score: 2003
Sequence: 1 gttgctctggcgagccaaag.....attgctctgtgattgttca 2003

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues 524120

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/5D_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/6_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
7: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2003	100.0	2003	5	US-08-468-011A-1
2	2003	100.0	2003	6	PCT-US93-07085-1
3	452.6	22.6	1862	1	US-07-864-249A-1
4	452.6	22.6	1862	3	US-07-864-249A-2
5	452.6	22.6	1863	1	US-07-864-249A-3
6	452.6	22.6	1863	3	US-07-864-249A-4
7	445.2	22.2	2051	1	US-08-468-475A-1
8	445.2	22.2	2051	3	US-08-468-475A-2
9	430.4	21.5	2010	1	US-08-468-475A-3
10	430.4	21.5	2010	3	US-08-468-475A-4
11	156.2	7.8	1377	1	US-08-112-817C-1
12	118.8	5.9	1401	3	US-08-855-213-32
13	118.8	5.9	1401	3	US-08-855-213-32
14	118.8	5.9	1869	3	US-08-855-213-40
15	118.8	5.9	1869	3	US-08-855-213-40
16	115.2	5.8	2112	5	US-08-811-897A-31
17	105	5.2	1455	3	US-08-855-213-31
18	105	5.2	2730	3	US-08-811-897A-39
19	105	5.2	2730	3	US-08-855-213-39
20	103.6	5.2	1380	2	US-08-110-286A-1
21	103.6	5.2	3035	6	PCT-US94-09235-1
22	100.2	5.0	1575	3	US-08-811-897A-34
23	100.2	5.0	1575	3	US-08-855-213-34
24	100.2	5.0	1664	3	US-08-811-897A-42
25	100.2	5.0	1664	3	US-08-855-213-42
26	100.2	5.0	1664	3	US-08-855-213-42

27	99.2	5.0	1514	2	US-08-381-433A-1	Sequence 1, Appli
28	99.2	5.0	1626	2	US-08-381-433A-3	Sequence 3, Appli
29	97.2	4.9	1248	2	US-08-110-286A-5	Sequence 5, Appli
30	97.2	4.9	1862	5	US-09-238-956-14	Sequence 1, Appli
31	97.2	4.9	1875	2	US-08-453-631-14	Sequence 14, Appli
32	97.2	4.9	1875	2	US-08-086-631-14	Sequence 14, Appli
33	97.2	4.9	1875	4	US-08-452-930-14	Sequence 14, Appli
34	97.2	4.9	1875	6	PCT-US93-0817A-14	Sequence 7, Appli
35	96.4	4.8	1468	2	US-08-381-433A-7	Sequence 1, Appli
36	96.4	4.8	3012	1	US-08-453-742-1	Sequence 1, Appli
37	96.4	4.8	3012	1	US-08-454-464-1	Sequence 1, Appli
38	96.4	4.8	3012	1	US-08-453-222-1	Sequence 1, Appli
39	96.4	4.8	3012	1	US-08-453-742-26	Sequence 26, Appli
40	96.4	4.8	3390	1	US-08-454-464-26	Sequence 26, Appli
41	96.4	4.8	3390	1	US-08-453-222-26	Sequence 26, Appli
42	96.4	4.8	3390	1	US-08-452-802-26	Sequence 24, Appli
43	96.4	4.8	3416	1	US-08-453-742-24	Sequence 24, Appli
44	96.4	4.8	3416	1	US-08-454-464-24	Sequence 24, Appli
45	96.4	4.8	3416	1	US-08-454-464-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1
US-08-468-011A-1
Sequence 1, Application US/08468011A
Patent No. 6030804
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Yi, Li
APPLICANT: Rosen, Steven
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: HUTDGT4
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2003 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-468-011A-1

Query Match 100.0%; Score 2003; DB 5; Length 2003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttgcctgggagcccaagttggaatattggaagcttttccgggctctggaagaggtt 60
 Db 1 GTTTGCTCTGGCAGCCAAAGTTGGCATATGGAAGCTTTTTCGGGCTCTGGAGGAGGT 60
 QY 61 ccttgcttcttctacagccgttcggggcatgacctgagggcgctgcgcctccagctct 120
 Db 61 CCCTGCTTCTCTACAGCCGTTCGGGCGATGGCTGGCTGGGGCGCTGCTCCACGCTCT 120
 QY 121 ggggttggctaagctcgcagctgctcctgcccagagccagctgagcttctgagcca 180
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 QY 361 algaactcaacca laaaggagttgcttccgacactgtaccccaalggaaacatgggatt 420
 Db 361 ATGACTTCAACCATTAAGGAGTTGCTTTTCGACACTGTAAACCCCAATGGAACATGGGATT 420
 QY 421 ttatgcacagcttaaa laaaaca tggggcaattatcagactgcttcttctcagc 480
 Db 421 TTATGCACAGCTTAATAAACAATGGGCCAATTAATTCAGACTGCCCTTCGCTTCTCGAC 480
 QY 481 cagatacagataggaagcaagaattctgtgaagccctctctgttaattataccgttg 540
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 QY 541 gctactccatctcttggcttcccttggctgtggctattctcatcattggttaactcaag 600
 Db 541 GCTACTCAATCTCTTTTGGTTCCCTTGGCTGTGGCTATTCTCATCATTTGGTTACTTTCAGAC 600
 QY 601 gattgcattgcactaggaactatatccacatgcacttatttggcttcttctatgctgagag 660
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 QY 961 ttgcagcatgggctgtggcagcagcaactctggctgatcgagggtgctgggaacttagtg 1020
 Db 961 TTGCAGCATGGGCTGTGGCAGGAGCAACTCTGGCTGATGCGAGGTGCTGGGAACCTTAGTG 1020
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RESULT 2

PCT-US95-07085-1

; Sequence 1, Application PC/TUS9507085

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R

; APPLICANT: Yi, Li

; APPLICANT: Rosen, Craig A

; APPLICANT: Ruben, Steven

QY 1081 tctgtttctgaataacggttagagttctagctaccaaaatctgggagaccatcgagttg 1140
 Db 1081 TTTCTGTTTCTGAATACGGTTAGAGTTCTAGCTTACCAAAATCTGGGAGACCAATGCGATTG 1140
 QY 1141 ggcatacacaaggaagcaatacaggaactgccaactgcacactgcctggttcctag 1200
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 Db 1201 TCTTTTGAGTGCAATACATCGTGTGCTGCTGCTCCTCCTTCTTCTTCTTCTTCTTCTTCT 1260
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 QY 1321 tcatctactgctactgcaatggagaggttcaggcacagctgaagaagatgtgagtcggt 1380
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 QY 1681 ggcctatggaatcttaaccacagactgaagatgacaaggagaagaaactgaggtattctct 1740
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 QY 1861 taatagtttttaggctccatgaattggctcctgtaaaaataactaacatgaaatgcaag 1920
 Db 1861 TAATAGTTTTTAGGCTCCCATGAATTTGGCTCCTGTAAATTAACGACATGAAAAATGCAAG 1920
 QY 1921 tgcataagagtagttatttactccttattggatcacaagtttctcctctctctctctctctct 1980
 Db 1921 TGCTAATGGAGTAGTTTATTAACCTTCTATTGGCATCAAGTTTTTCTCTCTAAATTAATGTAT 1980
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 Db 1981 GGTATTTGCTCTGTGATGTTCA 2003

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Qy	1621	ggagcaacaaggaaagatagtgggaggcagagagatgatatcttaataaggaaagccttccca	1680
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Qy	1681	ggcctatggaaacctaacccagacactgaaggatgacaaggagaaactgagagatgttctct	1740
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Qy	1741	gaatgacatgtgtggctgaacttcatgggctgtgtccaatggctgtgtgtgagagggc	1800
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Qy	1801	tggcctgatactcctatgcttgagcacaaggctgaaattcagttaagtggttactata	1860
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Qy	1861	taatagtttttaggctccatgaattggctcctgtaaatactaacgacatgaaaaatgcgaag	1920
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Qy	1921	tgtcaatggagtagtttataactctctattggcatacaagtttctctctaaataatgtat	1980
Db	1921	TGTCAATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTTCTCTTAAATTAATGTAT	1980
Qy	1981	ggtaattgctctgtgattgtcca	2003
Db	1981	GGTATTTGCTCTGTGATTTCTTCA	2003

RESULT 3
US-07-864-475A-1

? PARENT NO.: 3434800
 ?
 ? GENERAL INFORMATION:
 ?
 ? APPLICANT: Segre, Gino V.
 ? APPLICANT: Kronenberg, Henry M.
 ? APPLICANT: Abou-Samra, Abdul-Badi
 ? APPLICANT: Juppner, Harald
 ? APPLICANT: Potts, John T. [Jr.]
 ? APPLICANT: Schipani, Ernestina
 ? TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
 ? TITLE OF INVENTION: AND DNA ENCODING SAME
 ? NUMBER OF SEQUENCES: 17
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Fish & Richardson
 ? STREET: 225 Franklin Street
 ? CITY: Boston
 ? STATE: Massachusetts
 ? COUNTRY: U.S.A.
 ? ZIP: 02110-2804
 ?
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? COMPUTER: IBM PS/2 Model 502 or 555x
 ? OPERATING SYSTEM: MS-DOS (Version 5.0)
 ? SOFTWARE: Wordperfect (Version 5.1)
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/07/864,475A
 ? FILING DATE: 04-06-1992
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 07/681,702
 ? FILING DATE: 05-04-1991
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Paul T. Clark
 ? REGISTRATION NUMBER: 30,162
 ? REFERENCE/DOCKET NUMBER: 00786/071002
 ? TELECOMMUNICATION INFORMATION:
 ?

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2051 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1846
US-08-468-249A-3

Query Match 22.2%; Score 445.2; DB 3; Length 2051;
Best Local Similarity 62.9%; Pred. No. 3.7e-133;
Matches 744; Conservative 0; Mismatches 423; Indels 15; Gaps 3;
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DB 383 GAGGGCTCCCTGTCGCCGAGTGGGACAACTGCTTGTGTCCTATAGGGCCACG 442
QY 325 ggaataatcgctgttccatgcctccttattttatgacttcaaccataaaggattg 384
DB 443 GTGAAGTGGTGGCAGTACCTTGTCCCGATTACATTTATGACTTCAATCACAAAGGCCATG 502
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QY 565 tggctgtggtatcttcacatcattgttacttcagaagattgcttgcactagaactata 624
DB 677 TCACGGTGGCTGTCTCATCTCGCTCTATTTAGCGCGCTGCTACGCGCAACTACA 736
QY 625 tccacatgaacttattgttcttcttcacatgctgagagctacaagcatcttggtaagaaca 684
DB 737 TCCACATGACATGTTCTCTCTGCTTTATGCTGCGCGCGGAGCATCTTCTGTAAGGACG 796
QY 685 gagttagtccatgctcactatgaggaagagctggagctccctaaataatcagagatgacc 744
DB 797 CTGTGCTCTACTTGGCTTCCACGCTGGATGAGCGCGGAGCCCTCACAGAGAGAGTTCG 856
QY 745 cacaaaattccattgagggaactcttctgtggacaatc-----acaatatctgggtgca 798
DB 857 ACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCGCGGTAGGCTACGCTGGCTGCC 916
QY 799 agattgctgtgtgatttatttacttctcctggctacaataattatttggatcctgggtg 858
DB 917 GCGTGGCGGTGACCTTCTCTCTACTTCTCTGCTTCTGCTGCTACCAACTACTTCTGATTCTGTTGG 976

QY 859 aaggtctctacatgcataaatactcatttggcttcttttttcggacacacaaatcacctgt 918
DB 977 AGGGCTGTACTTGCACAGCCTCATCTTCATGGCTTTTTCAGAGAGAGAGTACCTGT 1036
QY 919 ggggtctcatctttagtaggtggtgggtttccagcagcaatttggcagcatgggtgtg 978
DB 1037 GGGCTTTCACCATTTTGGTGGGTGTACCGGCTCTCTTGGTGGCTGTGTTGGTGGGTG 1096
QY 979 cagcagcaactctggtgagtgctgggaacttagtgctggagacataagtgga 1038
DB 1097 TCAGAGCAACTTGGCCAACTGCTGGGATCTGAGCTCCGGGCACAAAGAGTGA 1156
QY 1039 ttatcaagcaccgatcttagcagctattgggtggaattttattcttcttctgaatacgg 1098
DB 1157 TCATCCAGGTGCCCATCTCTGGCATCTGTGTGCTCAACTTCATCTTTTATCAACATCA 1216
QY 1099 ttagagtcttagtaccataaactctggagaccaatggagttggcagcatgacacaggaagc 1158
DB 1217 TCCGGGTGCTTGGCACTAAGCTTCGGGAGACCAATGGGGCGGCTGTACACACGAGCAG 1276
QY 1159 aatacagaaactggccaaatcgacactggctcctggctccttagtcttggagtgcatata 1218
DB 1277 AGTACCGGAAGCTGCTCAGGTCCACGTTGGTGTCTGCTGGCTCTTGGTGTCCACTACA 1336
QY 1219 tctgttctgtgctgctcctcactcc---ttcactggggtcgtgggtggagatccgcatgc 1275
DB 1337 CCGTCTTCATGGCTTGGCGTACACCGAGGTCTCAGGGACATTTGGCAGATCCAGATGC 1396
QY 1276 actgtgagctcttctcaactccttccagggttcttcttggctctatcctatctactgtact 1335
DB 1397 ATTATGAGATGCTCTCAACTCTCTCCAGGATTTTGTGTGCCATCATATATCTTCT 1456
QY 1336 gcaatgagaggttcagcagagtggaagaatgtagagtcggtggaatctctccgtg 1395
DB 1457 GCAATGTGTGAGTGCAGCGAGAGATTAGGAAGTCATGAGCGCTGGACACTTGGCTGG 1516
QY 1396 actggaagaaagacaccgcccatgtgagcgcagatcggtc 1437
DB 1517 ACTTCAAGCGCAAGACGAGGTGGAGTAGACGACTACAGCT 1558
RESULT 9
US-07-864-475A-4
Sequence 4, Application US/07864475A
Patent No. 5494806
GENERAL INFORMATION:
APPLICANT: Segre, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF INVENTION: AND DNA ENCODING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,475A
FILING DATE: 04-06-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2010
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-07-864-475A-4

Query Match      21.5%; Score 430.4; DB 1; Length 2010;
Best Local Similarity 62.2%; Pred. No. 2,1e-128;
Matches 734; Conservative 0; Mismatches 431; Indels 15; Gaps 3;

QY 276 tgtttccctgaatggagtgactcatttggcccgagaggaacagtggggaaaaatatcg 335
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Db 349 TGTCTCGCGGAATGGACACACATCTCTGTCTGGCCGCTGGGGGCACCAAGTGAGGTGGTG 408

QY 336 gctgttccatgcccctcttatattatgacttcaaccataaaggagtgctttccgaacac 395
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Db 409 GCTGTGCCCTGTGCCGACTACACTTATGACTTCAATCACAAAGGCCATGCCATCCGACGC 468

QY 396 tgtaaccccaatggaaatggattttatgacagctttaaataaaacatgggccaaattat 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 469 TGTGACCGCAATGGCAGCTGGGAGCTGTGCTGGCCACACAGGACGTGGGCCAACTAC 528

QY 456 tcagactgccttgcttctgcagccagatatacagcataggaagaacaagaattctgtgaa 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 529 AGCGAGTGTCTCAAAATTTCTCAACCAATGA- ----CACTCGTGAACGGGAGGTGTTTGAC 582

QY 516 cgcctctatgtaatgataccgttggtgactccatctcttggcttccttggctggtgct 575
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Db 583 CGCCTGGGCATGATTTACACCTGGGCTACTCCGCTGCTGGCGTCCCTCACCCGTAGCT 642

QY 576 attctcatctatgttacttcagaacatgtgcttgcactaggaactatatccacatgcac 635
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Db 643 GTGCTCATCTGCGCTACTTTAGGCGGGCTGCACTGCACGCGCACTACATCCACATGCAC 702

QY 636 ttatttgttcttctatgtgagagctacaagcatctttgtcacaagacagagtagtccat 695
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Db 703 CTGTTCTCTGCTTCTATGCTGGCGCGCTGAGCATCTTCTCAAGGACGCTGTGCTCTAC 762

QY 696 gctcacataggaagtaaaagagctggagtcctcctaataataatcagagatgaccccaaaattcc 755
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Db 763 TCTGGGCCACCGCTTGTAGGCTGAGCGCCCTCACCGAGGAGGAGCTGCGCGCCCATCGCC 822

QY 756 attg-----aggcaactctgtgggacaaatcacaaatatatcgggtgcaagattgctgt 809
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 823 CAGGCGCCCGCCGCTGCCACCGCGCTGCGGGCTACCGGGCTGCAGGGTGGCTGTG 882

QY 810 gtgatgtttattacttcctgggtacaaattattattggatcctggtggaaggtctctac 869
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 883 ACCTTCTCTTCTTACTTCTTGCCACCAACTACTACTGGATTCTGTTGGAGGGGCTGTAC 942

QY 870 ctgcaataatcctatcttggcttcttcttcggacacaaataacctgtggggcttcac 929
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 943 CTGCACAGCTCATCTTCTCATGCGCTTCTTCTCAGAGAAGAAGTACCTGTGGGCTTACA 1002

QY 930 ttgataggctgggggtttccagagacattgtgtcagcatggctgtgacagagcaact 989
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1003 GTCTTCGGCTGGGGTCTGCCGCTGCTCTGCTGGCTGTGTGGGTCTAGTCTCAGAGCTACC 1062

QY 990 ctggctgatgcagggtgctgggaacttagtctgggagacatcaagtggatttatcaagca 1049
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Db 1063 CTGGCCAACACGGGTGCTGGACTTTGAGCTCCGGGAACAAAAAGTGGATCATCCAGGTG 1122
QY 1050 ccgactcttagcagctattggcgtgaattttattctgttctgaataacggttagagttcta 1109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1123 CCCATCTGGCTCCATTGTGTCTCAACTTCATCCTCTTCATCAATATATCTCGGGTGCTC 1182
QY 1110 gctaccacaaatctgggagaccaatgcagttgggcatacacaaaggaagcaaatacagaaaa 1169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1183 GCCACCAACGACGGGAGACCAACGCGCGCGGTGTGACACACGCGGACGATACCGGAAG 1242
QY 1170 ctggccaaatgacactggctcctggctccttagtcttcttggagtgcaattacatcgttctcg 1229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1243 CTGCTCAAAATCCACGCTGGTGTCTATGCCCCCTCTTTGGCGTCCACTACATTTGTTTCATG 1302
QY 1230 tgcctgctcactcctcct---tcactgggctcggggtgggagatcccgatgcactgtgaagctc 1286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1303 GCCACACCATACACGAGGTCTCAGGGACGCTCTGGCAAGTCCAGATGCACATATGAGATG 1362
QY 1287 ttcttcaactcctttcagggtttcttctgtctatctactctactgtcaatggagag 1346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1363 CTCTTCAACTCTCTCCAGGATTTTGTGCGCAATCATATACTGTTCTTGCATGGCGAG 1422
QY 1347 gttcaggcagagtggaagaagatgtggagtgcgttggaatctctcctggagtggaagaaagg 1406
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Db 1423 GTACAAGCTGAGATCAAGAAATCTTTGGAGCGCGTGGACACTGGCACTGGACTTCAAAGCGA 1482
QY 1407 acacggcctatgtggcagccgagatgcgctcagtgctca 1446
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Db 1483 AAGGCACGACGGGGAGCAGCACTATAGCTACGGGCCCA 1522

RESULT 10
US-08-468-249A-4
; Sequence 4, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2010 base pairs
; TYPE: nucleic acid
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Db 641 TGGGCTGTAAAGCAGCGCGTGGTGTATTTATCCAGTACTGTGTATGGCCAACTTCTTCTGGC 700
QY 850 tctgggtgaaggtctctacctgcataactcatctttgtggcttctcttttcggacacca 909
Db 701 TCGTGGTGAGGCGCTCTACCTGCACACCTACTTGCCTGTCTTCTCTGAGCGGA 760
QY 910 aatactgtggtggtctctctatagtaggctggggtttccacagcagcatgttggcagcat 969
Db 761 AGTACTTCTGGGGGTACATATTCTGGCTGGGGGTGCCAGCAGCTTCATCATGTGTGT 820
QY 970 gggctgtgacagcaacactctgctgatgagctgctgggaacttagtgcgtggagaca 1029
Db 821 GGACCGCTCTCAGATCCATTTTGAGGATATGGATGCTGGGACACCAATCCACTCCTCAC 880
QY 1030 tcaagtggatttataagcagcagcttagcagctattggcgtgaattttatctgtttc 1089
Db 881 TGTGGTGGATCATAAAGGCCCCCTCCCTCGCCTCCATCTCTGTGTGAATTCATCTATTCA 940
QY 1090 tgaatcaggttagagttcttagtaccataaactctggagaccacacagttgggcatgaca 1149
Db 941 TTTCGATCATCGAATCTTGTGTTCAAGAACTGCGACCCCGAGATGTCGGGAAGATGACA 1000
QY 1150 caaggaagcaatacaggaagaaactggccaaactgacactggctcctagtcttcttgag 1209
Db 1001 ACAG---CCCATACTGAGAGACTAGCCAGTCCACTCTTCTGTGATGCCCTATTGGAG 1057
QY 1210 tgcattacatcgtgttcgtgtgctgcctcactcctcactggtcgtggtggagatcc 1269
Db 1058 TGCACCTACATCATGTTGCTTCTTCCCTGACAAATTTAAGGCC-----GAAGTGA 1108
QY 1270 gcatgcactgtgagctctcttcttcaactcctctcaggggtttcttgtgtctatctact 1329
Db 1109 AAATGGCTTTTCAGCTCATCGTGGGATCTTCCAGGGTGTGTGGTGCGCATCTCTACT 1168
QY 1330 gctactgcaatgagaggttcaggcagaggtgaaagaagatgtggagctgggtgaatc 1386
Db 1169 GCTTCTCAATGTTAGGTGCGAGGAGAGCTGCGGCGGAAGTGGCGGCGCTGGCACC 1225

RESULT 12

US-08-811-897A-32
; Sequence 32, Application US/08811897A
; Patent No. 5858787
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSOYA, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABAYA, Yugo
; APPLICANT: SHIMAMOTO, No. 5858787io
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,897A
; FILING DATE: 05-MAR-1997

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1401 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1401
US-08-811-897A-32

Query Match 5.9%; Score 118.8; DB 3; Length 1401;
Best Local Similarity 53.7%; Pred. No. 4.3e-28;
Matches 321; Conservative 0; Mismatches 262; Indels 15; Gaps 3;
QY 790 tgggtggaagattcgtgtgtgagtgatttatttaacttctcgtcctacaaattatttggga 849
Db 668 TGGAGTGGAAAGCTGTCATGGTTTCTTCCACTACTGCGTGGTGTCCAACTACTTCTTGGC 727
QY 850 tctgtggtaaggtctctacctgcataatctcatcttctgtgcttcttcttcggacacca 909
Db 728 TGTTTCATTGGAAGCCCTGTACCTTTTACACTGCTGCTGGTGGAGACCTTCTTCCCTGAGAGGA 787
QY 910 aatacctgtggggtctcatcttgataggtggggtttccacgacagcatttgttgagcat 969
Db 788 GATATTTCTACTGTTACACCATCATCGGCTGGGGGACACCTACTGTGTGTGTAACAGTGT 847
QY 970 ggggtgtggcagcagcaactcgtggtgagtgaggtgctgggaacttagtgcgtg---ag 1026
Db 848 GGGCTGTGCTGAGGCTCTATTTTGATGATGAGGATGCTGGGATATGAATGACAGCACAG 907
QY 1027 acatcaagtggatttatacagcagcagctcttagcagctattggcgtgaattttattctct 1086
Db 908 CTCTGTGTGGTGGTGATCAAAAGCCCGGTGGTGGCTCTATATAATGGTTAACTTTGTGCTTT 967
QY 1087 ttctgaatacaggttagagttcttagctaccataaactctgggagaccaatgcagttgggcatg 1146
Db 968 TCATCGGCATCATCATCATCTTGTACAGAACTGCAGTCCCGACAGACATGGGAGGCAACG 1027
QY 1147 acacaaggaagcaatacagaggaactggcacaactcagacactggtcctggtcctagttctg 1206
Db 1028 AGTCAGCATCTACTTACGG---CTGGCCCGCTCCACCCCTACTGCTCATCTCCACCTCTCG 1084
QY 1207 gagtgcattacatcgtgttcgtgtgcctcactcctcactgggtcgtgggtgggaga 1266
Db 1085 GAATCCACTACACAGTATTCGCCCTTCTCTCCAGAGAACTCA-----GCAAGAGGG 1135
QY 1267 tccgcatgcactgtgagctcttcttcaactccttccagggtttcttctgtctatcatct 1326
Db 1136 AAAGACTTGTGTTTGAGCTTGGGCTGGGCTCTCTCCAGGGCTTTGTGGTGGCTGTACTCT 1195
QY 1327 actgctactgcaatggagaggttcaggcagaggttgaagaagatgtggagctcgttgaaa 1384
Db 1196 ACTGCTTCTGTAATGGGAGGTACAGGCGAGAGATTAAAGAGAAATGGAGGAGCTGGAA 1253

RESULT 13

US-08-855-213-32
; Sequence 32, Application US/08855213
; Patent No. 5892004


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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1869 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: mat_peptide
;     LOCATION: 77..1477
;
US-08-811-897A-40

Query Match          5.9%; Score 118.8; DB 3; Length 1869;
Best Local Similarity 53.7%; Pred. No. 5.2e-28;
Matches 321; Conservative 0; Mismatches 262; Indels 15; Gaps 3;

QY 790 tcgggtgcaagattgctgttgatgtttatttacttctggtcacaattatttggga 849
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QY 850 tcttggtggaaggtctctacatgcataatctcatcttcttggcttcttcttcggacacca 909
   ||||| || || || || || || || || || || || || || || || || ||
Db 804 TGTTTCATTGAAGCCCTGTACCTCTTTTACACTGCTGCTGGTGAGACCTCTTCCCTGAGAGGA 863

QY 910 aatacctggtgggtctcatcttgatagctgggttttccacagcagcatttgttgcagcat 969
   ||||| || || || || || || || || || || || || || || || || ||
Db 864 GATATTTCTACTGTGTACACCATCATCGGCTGGGGGACACCTACTGTGTGTAACAGTGT 923

QY 970 gggctgtggaaggtctctacatgcataatctcatcttcttggcttcttcttcggacacca 1026
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Db 744 TGGAGTGC AAAAGCTGTCATGGTTTCTTCCACTACTGCGTGGTCCAACTACTTCTGGC 803

QY 850 tcttggtggaaggtctctacatgcataatctcatcttcttggcttcttcttcggacacca 909
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Db 804 TGTTTCATTGAAGCCCTGTACCTCTTTTACACTGCTGCTGGTGAGACCTCTTCCCTGAGAGGA 863

QY 910 aatacctggtgggtctcatcttgatagctgggttttccacagcagcatttgttgcagcat 969
   ||||| || || || || || || || || || || || || || || || || ||
Db 864 GATATTTCTACTGTGTACACCATCATCGGCTGGGGGACACCTACTGTGTGTAACAGTGT 923

QY 970 gggctgtggaaggtctctacatgcataatctcatcttcttggcttcttcttcggacacca 1026
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Db 924 GGGCTGTGCTGAGGCTCTATTTTTGATGTGACAGGATGCTGGGATATGAATGACAGCACAG 983

QY 1027 acatcaagtggatttatcaagcacccgacatcttagcagctattgggctgaatttattctgt 1086
   ||||| || || || || || || || || || || || || || || || || ||
Db 984 CTCTGTGGTGGGTGATCAAAAGCCCGTGGTGGCTCTATATATGTTACTTTGGCTTT 1043

QY 1087 ttctgaatacaggttagagttcttagctacacaaatctgggagaccatgcagttgggcatg 1146
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Db 1044 TCATCGGCATCATCATCATCTCTTTGTACAGAACTGCAGTCCCGACACATGGGAGGCAACG 1103

QY 1147 acacaagaagcaatcacaggaaactggccaaatcgacactggctcctggtccttagtctttg 1206
   ||||| || || || || || || || || || || || || || || || || ||
;
; TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF
;
; NUMBER OF SEQUENCES: 55
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,213
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
;
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1869 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: mat_peptide
;     LOCATION: 77..1477
;
US-08-855-213-40

Query Match          5.9%; Score 118.8; DB 3; Length 1869;
Best Local Similarity 53.7%; Pred. No. 5.2e-28;
Matches 321; Conservative 0; Mismatches 262; Indels 15; Gaps 3;

QY 790 tcgggtgcaagattgctgttgatgtttatttacttctggtcacaattatttggga 849
   ||||| || || || || || || || || || || || || || || || || ||
Db 744 TGGAGTGC AAAAGCTGTCATGGTTTCTTCCACTACTGCGTGGTCCAACTACTTCTGGC 803

QY 850 tcttggtggaaggtctctacatgcataatctcatcttcttggcttcttcttcggacacca 909
   ||||| || || || || || || || || || || || || || || || || ||
Db 804 TGTTTCATTGAAGCCCTGTACCTCTTTTACACTGCTGCTGGTGAGACCTCTTCCCTGAGAGGA 863

QY 910 aatacctggtgggtctcatcttgatagctgggttttccacagcagcatttgttgcagcat 969
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QY 1087 ttctgaatacaggttagagttcttagctacacaaatctgggagaccatgcagttgggcatg 1146
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QY 1147 acacaagaagcaatcacaggaaactggccaaatcgacacatgctcctggtccttagtctttg 1206
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Db 1104 AGTCCAGCATCTACTTACGG---CTGGCCCGCTCCACCCCTACTGCTCATPCCACACTCTTGG 1160

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QY 1327 actgctactgcaatgagagaggttcaggcagaaggtgaagaagatgtagagctcggtagaa 1384
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Db 1272 ACTGCTTCTGTAATGGGGAGGTACAGGCAAGATTAAGAGGAATTAAGAGGAGCTGGAA 1329

RESULT 15
US-08-855-213-40
; Sequence 40, Application US/08855213
; Patent No. 5892004
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: Ogi, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 589200410
;
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR
```



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Db 1104 AGTCCACGATCTACTTACGG---CTGGCCCGCTCCACCCCTACTGCTCTCATCCCACTCTTCG 1160
Qy 1207 gagtgcattacatcggtgttcgtgtgcctgcctcaactccttcaactgggctcggtgggaga 1266
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Qy 1267 tcegcatacactgtgagctcttcttcaactccttcaacttcagggtttcttctgtctatcatct 1326
Db 1212 AAAGACTTGTGTTTGTAGCTTGGGCTGGGCTCCTTCCAGGGCTTTGGTGGCTGCTACTCT 1271
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Search completed: November 15, 2000, 20:32:48
Job time: 3920 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2000, 14:29:52 ; Search time 1010.91 Seconds
(without alignments)
12250.508 Million cell updates/sec

Title: US-09-236-468A-1
Perfect score: 2003
Sequence: 1 gttgctctggcgagcccaag.....atttgctctgtgattgttca 2003

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Db 128 ACCTTGCCCAACACTGGGTGCTGGGACCTGAGCTCTGGGCACAAAGATGGATCATCCAG 187
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QY 1167 aaactggccaaaatcgacactggtctctgtagtcttggagtgcaatcacatcgtgttctc 1226
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QY 1227 gttgctgcctcaactcct--tcactggctcgggtggagatccgcactgcactgtgagc 1284
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QY 1285 tcttctcaactccttccaggggttcttctgtctatctactctactgcaatggag 1344
Db 428 TGCTCTCAACTCCTTCCAGGGATTTTGTTCCTCATATATACATGTTTCTGCAATGGTG 487
QY 1345 aggttcaggcagagggtgaagaagatggagtggtgggaattctctcgtggactggaaaa 1404
Db 488 AGGTGCAGGCAGAGATTAGGAAGTCTTGGAGCGCTGGACACTGGCATTTGGACTTCAAGC 547
QY 1405 ggcacgcgcattgtgagccgcagatcgagct 1437
Db 548 GTAAAGCACGAAGGTGGAGTAGCAGCTACAGCT 580

RESULT 4
LOCUS BE014986 542 bp mRNA EST 09-JUL-2000
DEFINITION 126918 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE014986
VERSION BE014986.1 GI:8276022
KEYWORDS EST.
SOURCE Pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 542)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCAGTCAGCAGC
Plate: 57 row: L column: 1
Seq primer: ATTAGCTGACACTATAG.
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source Location/Qualifiers
1..542
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORF6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,

BASE COUNT 99 a 159 c 139 g 145 t
ORIGIN
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Best Local Similarity 67.3%; Pred. No. 2.2e-61;
Matches 364; Conservative 0; Mismatches 174; Indels 3; Gaps 1;
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QY 860 aggtctcactgcataatctcatctcttggcttcttcttcgacacaaatcacctgtg 919
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QY 1100 tagagttctagctaccacaaatctgggagacaaatgcagttgggcatgacacaaaggagca 1159
Db 302 CCGGGTCTTGGCACCAGCTGCGGGAGACCAACGCGCGGTGTGACACGGCGCAGCA 361
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QY 1337 c 1337
Db 542 c 542
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LOCUS AL043796 258 bp mRNA EST 29-FEB-2000
DEFINITION DKFZp434P0227_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434P0227 5', mRNA sequence.
ACCESSION AL043796
VERSION AL043796.1 GI:5423180
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 258)
AUTHORS Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Bloecker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Bloecker H
MPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp434P0227) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source location/Qualifiers

1. .258
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp434P0227"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT 67 a 67 c 76 g 48 t

ORIGIN

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Best Local Similarity 99.6%; Pred. No. 1.7e-57;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1303 aggtttcttctgtctatctactgtctactgtcaatgagaggttcaggcagaggtga 1362

Db 14 AGGTTCTTGTCTATCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGTGA 73

QY 1363 agaagatgtggagtcggtggaattcttcgtggactggaaaagacacccgcatgtggca 1422

Db 74 AGAAGATGTGGAGTCGGTGGAAATCTCTCCGTGGACTCGAAAAGGACACCGCCATGTGGCA 133

QY 1423 gccacagatgcggctcagtgctcaccacgctgacgcacagcagcagcagtcacagg 1482

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QY 1483 tggcgg-cagcacacgcagtggtgtctatctctggcgaagtgccaagatgcgcagcagcag 1541

Db 194 TGGCGGCAGCAGCACACGCATGCTGTTATCTCTGCGCAAGCTGCCAAGATGCCAGCAGAC 253

QY 1542 agcct 1546

Db 254 AGCCT 258

RESULT 6

AQ724325 369 bp DNA GSS 14-JUL-1999
LOCUS HS_2107_AL_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2107 Col=11 Row=C, DNA sequence.

DEFINITION

ACCESSION AQ724325.1 GI:5483994

VERSION GSS.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 369)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc.Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

JOURNAL

99380589

MEDLINE

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

TITLE

The WashU-HMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu

Plate: 2107 row: C column: 11

Seq primer: M13 Reverse

Class: BAC ends

High quality sequence stop: 369.

source location/Qualifiers

1. .369
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/clone="Plate=2107 Col=11 Row=C"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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BASE COUNT 92 a 99 c 96 g 81 t 1 others

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Best Local Similarity 96.3%; Pred. No. 3.9e-54;

Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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QY 1405 ggaacccgcacatgagcagccagatgcgctcagtcagtcaccaccgtaacgcacagca 1464

Db 184 GGACACCCCATGTGGCAGCCGAGATCGCGTCTCAGTGTCTCACCACCGTGCAGCACAGCA 243

QY 1465 ccagcagccagtcacagtggtgagg-cagcacacagcagtggtcttatctcttgcaaaagctg 1523

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QY 1524 ccaagatgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1583

Db 304 CCAAGATCGCCAGCAGACAGCCTGACAGCCACATCACTTTACCTGTCTATGCTGTGGAGTC 363

QY 1584 actcag 1589

Db 364 ACTCCG 369

RESULT 7

AA240746 554 bp mRNA EST 12-MAR-1997
LOCUS mv37all.r1 Guaywoodford Beier mouse kidney day 0 Mus musculus cDNA clone IMAGE:657212 5' similar to gb:X68596 PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE (HUMAN); gb:X78936 M.musculus mRNA for parathyroid hormone/parathyroid hormone (MOUSE); mRNA sequence.

DEFINITION

ACCESSION AA240746

VERSION AA240746.1 GI:1865137

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 554)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Search completed: November 15, 2000, 19:45:57
Job time: 18965 sec

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